

# Bibliography

- Andersen, S. K., Olesen, K. G., Jensen, F. V. and Jensen, F. (1989), HUGIN--- a shell for building Bayesian belief universes for expert systems, *in* N. S. Sridharan, ed., 'Proceedings on the Eleventh International Joint Conference on Artificial Intelligence', Morgan Kaufmann, San Mateo, CA, pp. 1080–1085.
- Anderson, E. C. and Thompson, E. A. (1999), MCMC likelihoods for population genetics, *in* 'Proceedings of the 52nd Session of the International Statistical Institute', Vol. 3, pp. 347–348.
- Baum, L. E. (1972), An inequality and associated maximization technique in statistical estimation for probabilistic functions on Markov processes, *in* O. Shisha, ed., 'Inequalities-III; Proceedings of the Third Symposium on Inequalities. University of California Los Angeles, 1969', Academic Press, New York, pp. 1–8.
- Baum, L. E. and Petrie, T. (1966), Statistical inference for probabilistic functions of finite state Markov chains, *Annals of Mathematical Statistics* **37**, 1554–1563.
- Baum, L. E., Petrie, T., Soules, G. and Weiss, N. (1970), A maximization technique occurring in the statistical analysis of probabilistic functions on Markov chains, *Annals of Mathematical Statistics* **41**, 164–171.
- Bernstein, F. (1925), Zusammenfassende Betrachtungen über die erblichen Blutstrukturen des Menschen, *Zeitschrift für induktiv Abstammungs- und VererbungsLehre* **37**, 237–270. English translation in: *Selected contributions to the literature of blood groups and immunology (Dunsford Memorial). I. The ABO system*. U.S.Army Medical Research Laboratory; Fort Knox (1966).
- Besag, J. E., Green, P., Higdon, D. and Mengerson, K. (1995), Bayesian computation and stochastic systems, *Statistical Science* **10**, 3–66.
- Bickeböller, H. and Thompson, E. A. (1996a), Distribution of genome shared IBD by half sibs: approximation via the Poisson clumping heuristic, *Theoretical Population Biology* **50**, 66–90.
- Bickeböller, H. and Thompson, E. A. (1996b), The probability distribution of the amount of an individual's genome surviving to the following generation, *Genetics* **143**, 1043–1049.

- Boehnke, M. (1994), Limits of resolution of genetic linkage studies: implications for the positional cloning of human disease genes, *Am J Hum Genet* **55**, 379–390.
- Boehnke, M. and Cox, N. J. (1997), Accurate inference of relationships in sib-pair linkage studies, *American Journal of Human Genetics* **61**, 423–429.
- Botstein, D., White, R. L., Skolnick, M. H. and Davis, R. W. (1980), Construction of a linkage map in man using restriction fragment polymorphism, *American Journal of Human Genetics* **32**, 314–331.
- Broman, K. W. (1999), Cleaning genotypic data, *Genetic Epidemiology* **17**, Suppl. 79–83.
- Broman, K. W. and Weber, J. (2000), Characterization of human crossover interference, *American Journal of Human Genetics* **66**, 1911–1926.
- Browning, S. (1998), Relationship information contained in gamete identity by descent data, *Journal of Computational Biology* **5**, 323–334.
- Browning, S. (1999), Monte Carlo Likelihood Calculation for Identity by Descent Data, Ph.D. thesis, Department of Statistics, University of Washington.
- Browning, S. and Thompson, E. A. (1999), Interference in the analysis of genetic marker data, *American Journal of Human Genetics* **65**, Suppl. A244.
- Cannings, C., Thompson, E. A. and Skolnick, M. H. (1978), Probability functions on complex pedigrees, *Advances of Applied Probability* **10**, 26–61.
- Cannings, C., Thompson, E. A. and Skolnick, M. H. (1980), Pedigree analysis of complex models, in J. Mielke and M. Crawford, eds, ‘Current Developments in Anthropological Genetics’, Plenum Press, New York, pp. 251–298.
- Ceppelini, R., Siniscalco, M. and Smith, C. A. B. (1955), The estimation of gene frequencies in a random mating population, *Annals of Human Genetics* **20**, 97–115.
- Cotterman, C. W. (1974), A Calculus for Statistico-Genetics. Ph.D. Thesis 1940. Ohio State University, in P. A. Ballonoff, ed., ‘Genetics and Social Structure’, Academic Press, New York.
- Cottingham, R. W., Idury, R. M. and Schäffer, A. A. (1993), Faster sequential genetic linkage computations, *American Journal of Human Genetics* **53**, 252–263.
- Cox, T. K., Kerem, B., Rommens, J., Iannuzzi, M. C., Drumm, M., Collins, F. S., Dean, M. and et al. (1989), Mapping of the cystic fibrosis gene using putative ancestral recombinants, *American Journal of Human Genetics* **45** Suppl, A136.

- Dempster, A. P., Laird, N. M. and Rubin, D. B. (1977), Maximum likelihood from incomplete data via the EM algorithm (with Discussion), *Journal of the Royal Statistical Society, B* **39**, 1-37.
- Denniston, C. (1975), Probability and genetic relationship: two loci, *Annals of Human Genetics* **39**, 89-104.
- Donnelly, K. P. (1983), The probability that related individuals share some section of genome identical by descent, *Theoretical Population Biology* **23**, 34-63.
- Edwards, A. W. F. (1967), Automatic construction of genealogies from phenotypic information (AUTOKIN), *Bulletin of the European Society of Human Genetics* **1**, 42-43.
- Edwards, A. W. F. (1972), *Likelihood*, Cambridge University Press, Cambridge, UK.
- Elston, R. C. and Stewart, J. (1971), A general model for the analysis of pedigree data, *Human Heredity* **21**, 523-542.
- Fisher, R. A. (1922), The systematic location of genes by means of crossover observations, *American Naturalist* **56**, 406-411.
- Fisher, R. A. (1948), A quantitative theory of genetic recombination and chiasma formation, *Biometrics* **4**, 1-13.
- Geman, S. and Geman, D. (1984), Stochastic Relaxation, Gibbs Distributions, and the Bayesian Restoration of Images, *IEEE Transactions on Pattern Analysis and Machine Intelligence* **6**, 721-741.
- Geyer, C. J. (1991a), Markov chain Monte Carlo maximum likelihood., in E. M. Keramidas and S. M. Kaufman, eds, 'Computer Science and Statistics: Proceedings of the 23rd Symposium on the Interface', Interface Foundation of North America, Fairfax Station, VA, pp. 156-163.
- Geyer, C. J. (1991b), Reweighting Monte Carlo Mixtures, Technical Report 568, School of Statistics, Univ. of Minn.
- Geyer, C. J. (1992), Practical Markov chain Monte Carlo (with discussion), *Statistical Science* **7**, 473-511.
- Geyer, C. J. and Thompson, E. A. (1992), Constrained Monte Carlo maximum likelihood for dependent data, (with dicussion), *Journal of the Royal Statistical Society, B* **54**, 657-699.
- Geyer, C. J. and Thompson, E. A. (1995), Annealing Markov chain Monte Carlo with applications to ancestral inference, *Journal of the American Statistical Association* **90**, 909-920.
- Gilks, W. R., Richardson, S. and Spiegelhalter, D. J., eds (1996), *Markov Chain Monte Carlo in Practice*, Chapman and Hall, New York.

- Goddard, K. A., Yu, C. E., Oshima, J., Miki, T., Nakura, J., Piussan, C., Martin, G. M. and et al. (1996), Toward localization of the Werner syndrome gene by linkage disequilibrium and ancestral haplotyping: lessons learned from analysis of 35 chromosome 8p11.1-21.1 markers, *American Journal of Human Genetics* **58**, 1286-1302.
- Goldstein, D. R., Zhao, H. and Speed, T. P. (1995), Relative efficiencies of chi 2 models of recombination for exclusion mapping and gene ordering, *Genomics* **27**, 265-273.
- Graham, J. and Thompson, E. A. (1998), Disequilibrium likelihoods for fine-scale mapping of a rare allele, *American Journal of Human Genetics* **63**, 1517-1530.
- Green, P. J. (1995), Reversible jump Markov chain Monte Carlo computation and Bayesian model determination, *Biometrika* **82**, 711-732.
- Griffiths, R. C. and Tavaré, S. (1994a), Ancestral Inference in Population Genetics, *Statistical Science* **9**, 307-319.
- Griffiths, R. C. and Tavaré, S. (1994b), Simulating probability distributions in the coalescent, *Theoretical Population Biology* **46**, 131-159.
- Griffiths, R. C. and Tavaré, S. (1998), The age of a mutation in a general coalescent tree, *Stochastic Models* **14**, 273-295.
- Guo, S. W. and Thompson, E. A. (1992), A Monte Carlo method for combined segregation and linkage analysis, *American Journal of Human Genetics* **51**, 1111-1126.
- Guo, S. W. and Thompson, E. A. (1994), Monte Carlo estimation of mixed models for large complex pedigrees, *Biometrics* **50**, 417-432.
- Haldane, J. B. S. (1919), The combination of linkage values and the calculation of distances between the loci of linked factors, *Journal of Genetics* **8**, 229-309.
- Haldane, J. B. S. and Smith, C. A. B. (1947), A new estimate of the linkage between the genes for colour-blindness and haemophilia in man, *Annals of Eugenics* **14**, 10-31.
- Hammersley, J. M. and Handscomb, D. C. (1964), *Monte Carlo Methods*, Methuen and Co., London, UK.
- Harbron, C. (1995), A pedigree based algorithm for finding efficient peeling sequences, *I.M.A. Journal of Mathematics Applied in Medicine & Biology* **12**, 13-27.
- Harbron, C. and Thomas, A. W. (1994), Alternative graphical representations of genotypes in a pedigree, *I.M.A. Journal of Mathematics Applied in Medicine & Biology* **11**, 217-228.

- Hästbacka, J., de la Chapelle, A., Kaitila, I., Sistonen, P., Weaver, A. and Lander, E. (1992), Linkage disequilibrium mapping in isolated founder populations: diastrophic dysplasia in Finland, *Nature Genetics* **2**, 204-211.
- Hastings, W. K. (1970), Monte Carlo sampling methods using Markov chains and their applications, *Biometrika* **57**, 97-109.
- Heath, S. C. (1997), Markov chain Monte Carlo segregation and linkage analysis for oligogenic models, *American Journal of Human Genetics* **61**, 748-760.
- Heath, S. and Thompson, E. A. (1997), MCMC samplers for multilocus analyses on complex pedigrees, *American Journal of Human Genetics* **61**, A278.
- Henderson, C. R. (1976), A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values, *Biometrics* **32**, 69-83.
- Heuch, I. and Li, F. M. H. (1972), PEDIG--A computer program for calculation of genotype probabilities, using phenotypic information, *Clinical Genetics* **3**, 501-504.
- Hilden, J. (1970), GENEX -An algebraic approach to pedigree probability calculus, *Clinical Genetics* **1**, 319-348.
- Hoeschele, I. (1994), Bayesian QTL mapping via the Gibbs sampler, in 'Proc. 5th World Congr. Genet. Appl. Livst. Prod.', Vol. 21, Guelph, Canada, pp. 241-244.
- Hulten, M., Lawrie, N. M. and Laurie, D. A. (1990), Chiasma-based genetic map of chromosome 21, *American Journal of Medical Genetics Suppl.* **7**, 148-154.
- Irwin, M., Cox, N. and Kong, A. (1994), Sequential imputation for multilocus linkage analysis, *Proceedings of the National Academy of Sciences (USA)* **91**, 11684-11688.
- Jensen, C. S., Kjaerulff, U. and Kong, A. (1995), Blocking Gibbs sampling in very large probabilistic expert systems., *International Journal of Human-Computer Studies* **42**, 647-666.
- Jensen, C. S. and Kong, A. (1999), Blocking Gibbs sampling for linkage analysis in large pedigrees with many loops, *American Journal of Human Genetics* **65**, 885-901.
- Kaplan, N. L., Hill, W. G. and Weir, B. S. (1995), Likelihood methods for locating disease genes in nonequilibrium populations, *American Journal of Human Genetics* **56**, 18-32.
- Karigl, G. (1981), A recursive algorithm for the calculation of gene identity coefficients, *Annals of Human Genetics* **45**, 299-305.

- Karlin, S. and Liberman, U. (1979), A natural class of recombination processes and related measures of crossover interference, *Advances of Applied Probability* **11**, 479–501.
- Karunaratne, P. and Elston, R. (1998), Likelihood calculation conditional on observed pedigree structure, *American Journal of Human Genetics* **62**, 738–739.
- King, T. R., Dove, W. F., Guénet, J., Hermann, B. G. and Shedlovsky, A. (1991), Meiotic mapping of murine chromosome 17: The string of loci around *l(17)-2-Pas.*, *Mammalian Genome* **1**, 37–46.
- Kingman, J. F. C. (1982), The Coalescent, *Stochastic Processes* **13**, 235–248.
- Knott, S. and Haley, C. (1992), Maximum Likelihood Mapping of Quantitative Trait Loci Using Full-Sib Families, *Genetics* **132**, 1211–1222.
- Kong, A. (1991), Analysis of pedigree data using methods combining peeling and Gibbs sampling, in E. M. Keramidas and S. M. Kaufman, eds, ‘Computer Science and Statistics: Proceedings of the 23rd Symposium on the Interface’, Interface Foundation of North America, Fairfax Station, VA, pp. 379–385.
- Kong, A., Liu, J. and Wong, W. H. (1994), Sequential imputations and Bayesian missing data problems, *Journal of the American Statistical Association* **89**, 278–288.
- Kosambi, D. D. (1944), The estimation of map distances from recombination values, *Annals of Eugenics* **12**, 172–175.
- Kruglyak, L., Daly, M. J. and Lander, E. S. (1995), Rapid multipoint linkage analysis of recessive traits in nuclear families, including homozygosity mapping, *American Journal of Human Genetics* **56**, 519–527.
- Kruglyak, L., Daly, M. J., Reeve-Daly, M. P. and Lander, E. S. (1996), Parametric and nonparametric linkage analysis: a unified multipoint approach, *American Journal of Human Genetics* **58**, 1347–1363.
- Kruglyak, L. and Lander, E. S. (1998), Faster multipoint linkage analysis using Fourier transforms, *Journal of Computational Biology* **5**, 1–7.
- Kuhner, M. K., Yamato, J. and Felsenstein, J. (1995), Estimating effective population size and mutation rate from sequence data using Metropolis-Hastings sampling, *Genetics* **140**, 1421–1430.
- Kullback, S. and Leibler, R. A. (1951), On information and sufficiency, *Annals of Statistics* **22**, 79–86.
- Kumm, J., Browning, S. and Thompson, E. A. (1999), Validation of pedigree data in the presence of genotyping error, *American Journal of Human Genetics* **65**, Suppl. A???

- Lander, E. S. and Botstein, D. (1987), Homozygosity mapping: a way to map human recessive traits with the DNA of inbred children, *Science* **236**, 1567-1570.
- Lander, E. S. and Green, P. (1987), Construction of multilocus genetic linkage maps in humans., *Proceedings of the National Academy of Sciences (USA)* **84**, 2363-2367.
- Lange, K. (1997), *Mathematical and Statistical Methods for Genetic Analysis*, Statistics for Biology and Health, Springer Verlag, New York.
- Lange, K. and Matthyssse, S. (1989), Simulation of pedigree genotypes by random walks, *American Journal of Human Genetics* **45**, 959-970.
- Lange, K. and Sobel, E. (1991), A random walk method for computing genetic location scores, *American Journal of Human Genetics* **49**, 1320-1334.
- Lathrop, G. M., Lalouel, J. M. and Julier, C. and Ott, J. (1984), Strategies for multilocus linkage analysis in humans, *Proceedings of the National Academy of Sciences (USA)* **81**, 3443-3446.
- Lauritzen, S. J. (1992), Propagation of probabilities, means and variances in mixed graphical association models, *Journal of the American Statistical Association* **87**, 1098-1108.
- Liberman, U. and Karlin, S. (1984), Theoretical models of genetic map functions, *Theoretical Population Biology* **25**, 331-346.
- Lin, S. and Speed, T. P. (1996), Incorporating crossover interference into pedigree analysis using the  $\chi^2$  model, *Human Heredity* **46**, 315-322.
- Lin, S., Thompson, E. A. and Wijsman, E. M. (1993), Achieving irreducibility of the Markov chain Monte Carlo method applied to pedigree data, *I.M.A. Journal of Mathematics Applied in Medicine & Biology* **10**, 1-17.
- Lin, S., Thompson, E. A. and Wijsman, E. M. (1994), An algorithm for Monte Carlo estimation of genotype probabilities on complex pedigrees, *Annals of Human Genetics* **58**, 343-357.
- Long, A., Mullaney, S., Reid, L., Fry, J., Langley, C. and Mackay, T. (1995), High Resolution Mapping of Genetic Factors Affecting Abdominal Bristle Number in *Drosophila melanogaster*, *Genetics* **139**, 1273-1291.
- MacCluer, J. W., VandeBerg, J. L., Read, B. and Ryder, O. A. (1986), Pedigree Analysis by Computer Simulation, *Zoo Biology* **5**, 147-160.
- Mather, K. (1938), Crossing-over, *Biological Reviews of the Cambridge Philosophical Society* **13**, 252-292.

- Mendel, G. (1866), Experiments in Plant Hybridisation, in J. H. Bennett, ed., 'English translation and commentary by R. A. Fisher', Oliver and Boyd, Edinburgh, 1965.
- Meng, X. L. and Wong, W. H. (1996), Simulating ratios of normalizing constants via simple identity: A theoretical exploration, *Statistica Sinica* **6**, 831–860.
- Metropolis, N., Rosenbluth, A. W., Rosenbluth, M. N., Teller, A. H. and Teller, E. (1953), Equations of state calculations by fast computing machines, *Journal of Chemical Physics* **21**, 1087–1092.
- Morton, N. E. (1955), Sequential tests for the detection of linkage, *American Journal of Human Genetics* **7**, 277–318.
- Morton, N. E. and MacLean., C. J. (1974), Analysis of family resemblance. III. Complex segregation of quantitative traits, *American Journal of Human Genetics* **26**, 489–503.
- Ott, J. (1979), Maximum likelihood estimation by counting methods under polygenic and mixed models in human pedigrees, *American Journal of Human Genetics* **31**, 161–175.
- Ott, J. (1999), *Analysis of Human Genetic Linkage*, 3 rd. ed., The Johns Hopkins University Press, Baltimore, MD.
- Ploughman, L. M. and Bochnke, M. (1989), Estimating the power of a proposed linkage study for a complex genetic trait, *American Journal of Human Genetics* **44**, 543–551.
- Rannala, B. and Slatkin, M. (1998), Likelihood analysis of disequilibrium mapping, and related problems, *American Journal of Human Genetics* **62**, 459–473.
- Redner, R. A. and Walker, H. F. (1984), Mixture Densities, Maximum Likelihood and the EM Algorithm, *SIAM Review* **26**, 195–202.
- Remmers, E. F., Du, Y., Ding, Y. P., Kotake, S., Ge, L., Zha, H., Goldmuntz, E. A., Hansen, C. and Wilder, R. L. (1996), Localization of the gene responsible for the op (osteopetrosis) defect in rats on chromosome 10, *Journal of Bone and Mineral Research* **11**, 1856–1861.
- Robbins, R. B. (1918), Some applications of mathematics to breeding problems. III, *Genetics* **3**, 375–389.
- Satagopan, J. M., Yandell, B. S., Newton, M. A. and Osborn, T. C. (1996), A Bayesian approach to detect quantitative trait loci using Markov chain Monte Carlo., *Genetics* **144**, 805–816.
- Sheehan, N. A. (1990), Genetic Restoration on Complex Pedigrees, Ph.d. thesis, Department of Statistics, University of Washington.

- Sheehan, N. A. and Thomas, A. W. (1993), On the irreducibility of a Markov chain defined on a space of genotype configurations by a sampling scheme, *Biometrics* **49**, 163–175.
- Smith, C. A. B. (1953), Detection of linkage in human genetics, *Journal of the Royal Statistical Society, B* **15**, 153–192.
- Sobel, E. and Lange, K. (1993), Metropolis sampling in pedigree analysis, *Statistical Methods in Medical Research* **2**, 263–282.
- Sobel, E. and Lange, K. (1996), Descent graphs in pedigree analysis: Applications to haplotyping, location scores, and marker-sharing statistics, *American Journal of Human Genetics* **58**, 1323–1337.
- Sorensen, D. A., Andersen, S., Gianola, D. and Korsgaard, I. R. (1995), Bayesian inference in threshold models using Gibbs sampling, *Genetics Selection Evolution* **27**, 229–249.
- Speed, T. (1996), What is a genetic map function?, in T. Speed and M. S. Waterman, eds, 'Genetic Mapping and DNA Sequencing', Vol. 81 of *IMA Volumes in Mathematics and its Applications*, Springer-Verlag, New York, pp. 65–88.
- Stephens, M. and Donnelly, P. (2000), Inference in molecular population genetics (with Discussion), *Journal of the Royal Statistical Society, B* **62**, in press.
- Sturt, E. (1976), A mapping function for human chromosomes, *Annals of Human Genetics* **40**, 147–163.
- Thompson, E. A. (1974), Gene identities and multiple relationships, *Biometrics* **30**, 667–680.
- Thompson, E. A. (1981), Pedigree analysis of Hodgkin's disease in a Newfoundland genealogy, *Annals of Human Genetics* **45**, 279–292.
- Thompson, E. A. (1986), *Pedigree Analysis in Human Genetics*, Johns Hopkins University Press, Baltimore.
- Thompson, E. A. (1988), Two-locus and three-locus gene identity by descent in pedigrees, *I.M.A. Journal of Mathematics Applied in Medicine & Biology* **5**, 261–280.
- Thompson, E. A. (1991), Probabilities on complex pedigrees: the Gibbs sampler approach, in E. M. Keramidas and S. M. Kaufman, eds, 'Computer Science and Statistics: Proceedings of the 23rd Symposium on the Interface', Interface Foundation of North America, Fairfax Station, VA, pp. 321–328.
- Thompson, E. A. (1994a), Monte Carlo estimation of multilocus autozygosity probabilities, in J. Sall and A. Lehman, eds, 'Proceedings of the 1994 Interface conference', Fairfax Station, VA, pp. 498–506.

- Thompson, E. A. (1994b), Monte Carlo likelihood in genetic mapping, *Statistical Science* **9**, 355–366.
- Thompson, E. A. (1994c), Monte Carlo likelihood in the genetic mapping of complex traits, *Philosophical Transactions of the Royal Society of London (Series B)* **344**, 345–351.
- Thompson, E. A. (1997), Conditional gene identity in affected individuals, in I. H. Pawlowitzki, J. H. Edwards and E. A. Thompson, eds, 'Genetic Mapping of Disease Genes', Academic Press, London, pp. 137–146.
- Thompson, E. A. (2000a), MCMC estimation of multi-locus genome sharing and multipoint gene location scores, *International Statistical Review* **68**, 53–73.
- Thompson, E. A. (2000b), Monte Carlo methods on Genetic Structures, in O. E. Barndorff-Nielsen, D. R. Cox and C. Klüppelberg, eds, 'Complex Stochastic Systems', Séminaire Européen de Statistique, Chapman and Hall, London, UK, pp. 179–222:in press.
- Thompson, E. A. and Guo, S. W. (1991), Evaluation of likelihood ratios for complex genetic models, *I.M.A. Journal of Mathematics Applied in Medicine & Biology* **8**, 149–169.
- Thompson, E. A. and Heath, S. C. (1999), Estimation of conditional multilocus gene identity among relatives, in F. Scillier-Moiseiwitsch, ed., 'Statistics in Molecular Biology and Genetics: Selected Proceedings of a 1997 Joint AMS-IMS-SIAM Summer Conference on Statistics in Molecular Biology', IMS Lecture Note–Monograph Series Volume 33, Institute of Mathematical Statistics, Hayward, CA, pp. 95–113.
- Thompson, E. A., Kravitz, K., Hill, J. and Skolnick, M. H. (1978), Linkage and the power of a pedigree structure, in N. E. Morton, ed., 'Genetic Epidemiology', Academic Press, New York, pp. 247–253.
- Thompson, E. A. and Meagher, T. R. (1998), Genetic linkage in the estimation of pairwise relationship, *Theoretical and Applied Genetics* **97**, 857–864.
- Thompson, E. A. and Morgan, K. (1989), Recursive descent probabilities for rare recessive lethals, *Annals of Human Genetics* **53**, 357–374.
- Thompson, E. A. and Shaw, R. G. (1990), Pedigree analysis for quantitative traits: Variance components without matrix inversion, *Biometrics* **46**, 399–414.
- Thompson, E. A. and Shaw, R. G. (1992), Estimating polygenic models for multivariate data on large pedigrees, *Genetics* **131**, 971–978.
- Weeks, D. E., Lathrop, G. M. and Ott, J. (1993), Multipoint mapping under genetic interference., *Human Heredity* **43**, 86–97.
- Weinberg, W. (1912), Zur Vererbung der Anlage der Bluterkrankheit mit methodol. Ergänzungen meiner Geschwistermethode, *Arch. Rass. u. GesBiol.* **9**, 694–709.

- Weinstein, A. (1936), The theory of multiple-strand crossing over, *Genetics* **21**, 155–199.
- Weir, B. S. (1996), *Genetic Data Analysis II*, Sinauer Associates, Inc., Sunderland, MA.
- Whittemore, A. S. and Tu, I.-P. (1998), Simple, Robust Linkage Tests for Affected Sibs, *American Journal of Human Genetics* **62**, 1228–1242.
- Wright, S. (1922), Coefficients of inbreeding and relationship, *American Naturalist* **56**, 330–338.
- Wright, S. and McPhee, H. C. (1925), An approximate method of calculating coefficients of inbreeding and relationship from livestock pedigrees, *Journal of Agricultural Research* **31**, 377–383.
- Zeng, Z. (1994), Precision Mapping of Quantitative Trait Loci, *Genetics* **136**, 1457–1468.
- Zhao, H., Sped, T. P. and McPeek, M. S. (1995), Statistical analysis of crossover interference using the chi-square model, *Genetics* **139**, 1045–1056.

## Cited web sites

- <http://linkage.rockefeller.edu/soft/list.html>  
The Rockefeller Genetic Linkage Software list
- <http://www.stat.washington.edu/thompson/Genepi/pangaea.shtml>  
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